## SEQUENCE LISTING

```
<110> David J. Glass
 <120> ION CHANNEL RECEPTOR AND USES THEREOF
 <130> REG 860A
 <140> Not Yet Known
 <141> Filed Herewith
 <150> 60/397,290
 <151> 2003-07-19
<160> 4
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 1837
<212> DNA
<213> human
<400> 1
gactcactat agggcggccg cgaattcggc accagcacca ccggagtggg ctccgtgggt 60
gctggggcag gagtttcctc actccccgcc tggccgtcgc tcctccgctg actccgcgcc 120
cttctacggg ccgtctccca ccctctgagc ggacgcaggg agtcgatgcc gggcgaaccg 180
ggcgccatga agggcagctg cctaacgggc gccgcggcgg aggggctggc cggctgaggg 240
cccgcgctgg gccgaggcat gcggagcccg ggcgggatcc tgctccaggc gctgcccgg 300
ctgctgcagc acgccgcct cccgggcctc gccgagctgc cggcccgctg ggccctgccg 360
cggggtgcgg gcggggacgg cccggcggac cgccttcccc gcgggggcgg ggcgagcgcg 420
gcggcggcag cagcggcggc ctcgggcgcc ctgctcggcg cctatctgga gcgccacggt 480
ccgcccgagg cttcggagct gccggagccg ggcggggcct tggcgggcgg ccccgggagt 540
ggcggcggcg gcgtggtggt cggcgtggct gaggtgagaa actggcgctg ctgctgcctc 600
ggcagcacct gttggtgccg gagcctcgtg ctggtctgcg tgttggccgc cctgtgcttc 660
gcttccctgg ccctggtccg ccgctacctt caccacctcc tgctgtgggt ggagagcctt 720
gactcgctgc tgggggtcct gctcttcgtc gtgggcttca tcgtggtctc tttcccctgc 780
ggctggggct acatcgtgct caacgtggcc gctggctacc tgtacggctt cgtgctgggc 840
atgggtctga tgatggtggg cgtcctcatc ggcaccttca tcgcccatgt ggtctgcaag 900
cggctcctca ccgcctgggt ggccgccagg atccagagca gcgagaagct gagcgcggtt 960
attcgcgtag tggagggagg aagcggcctg aaagtggtgg cgctggccag actgacaccc 1020
ataccttttg ggcttcagaa tgcagtgttt tcgattactg atctctcatt acccaactat 1080
ctgatggcat cttcggttgg actgcttcct acccagcttc tgaattctta cttgggtacc 1140
accctgcgga caatggaaga tgtcattgca gaacagagtg ttagtggata ttttgtttt 1200
tgtttacaga ttattataag tataggcctc atgttttatg tagttcatcg agctcaagtg 1260
gaattgaatg cagctattgt agcttgtgaa atggaactga aatcttctct ggttaaaggc 1320
aatcaaccaa ataccagtgg ctcttcattc tacaacaaga ggaccctaac attttctgga 1380
ggtggaatca atgttgtatg attctaatga gatacgtgat tgtcaagagc ctagtgtgct 1440
atctaaggtc tagcagtcac ttcactagtg ggcagagaca agttctaatt gtattacagc 1500
acaaacaaaa ctgactagtt tttaaattgc acaatttttt ttttttaaag caagaatcat 1560
tttctgggta tgtaagtgta aatgtagatg caaatttggc tgcacctctt tatcatgcct 1620
gtattggcct ataggtctgc actttagtgt tttttaattg ttttatttct gtgtatttac 1680
gaacagagaa ataacccaaa tattatttct gcttagtgtc tttatttata aagcccatga 1740
gtagtttgta tgcatctttc ctacttgtaa agatgagtaa aagtatgcag ttttaaattt 1800
ataatattat tggatgttct ttgctttggt agtcttt
                                                                  1837
```

```
<211> 376
<212> PRT
<213> human
<400> 2
Met Arg Ser Pro Gly Gly Ile Leu Leu Gln Ala Leu Pro Arg Leu Leu
                                    10
Gln His Ala Ala Leu Pro Gly Leu Ala Glu Leu Pro Ala Arg Trp Ala
            20
                                25
Leu Pro Arg Gly Ala Gly Gly Asp Gly Pro Ala Asp Arg Leu Pro Arg
                           40
Gly Gly Gly Ala Ser Ala Ala Ala Ala Ala Ala Ala Ser Gly Ala
                       55
Leu Leu Gly Ala Tyr Leu Glu Arg His Gly Pro Pro Glu Ala Ser Glu
                    70
                                       75
Leu Pro Glu Pro Gly Gly Ala Gly Gly Pro Gly Ser Gly Gly Gly
               85
                                  90
                                                        95
Val Val Gly Val Ala Glu Val Arg Asn Trp Arg Cys Cys Leu
           100
                               105
                                                   110
Gly Ser Thr Cys Trp Cys Arg Ser Leu Val Leu Val Cys Val Leu Ala
                           120
                                               125
Ala Leu Cys Phe Ala Ser Leu Ala Leu Val Arg Arg Tyr Leu His His
                       135
Leu Leu Leu Trp Val Glu Ser Leu Asp Ser Leu Leu Gly Val Leu Leu
                   150
Phe Val Val Gly Phe Ile Val Val Ser Phe Pro Cys Gly Trp Gly Tyr
               165
                                   170
Ile Val Leu Asn Val Ala Ala Gly Tyr Leu Tyr Gly Phe Val Leu Gly
           180
                               185
Met Gly Leu Met Met Val Gly Val Leu Ile Gly Thr Phe Ile Ala His
       195
                          200
Val Val Cys Lys Arg Leu Leu Thr Ala Trp Val Ala Ala Arg Ile Gln
                       215
                                           220
Ser Ser Glu Lys Leu Ser Ala Val Ile Arg Val Val Glu Gly Gly Ser
                  230
                                       235
Gly Leu Lys Val Val Ala Arg Leu Thr Pro Ile Pro Phe Gly Leu Gln
               245
                                   250
Asn Ala Val Phe Ser Ile Thr Asp Leu Ser Leu Pro Asn Tyr Leu Met
           260
                               265
Ala Ser Ser Val Gly Leu Leu Pro Thr Gln Leu Leu Asn Ser Tyr Leu
       275
                           280
Gly Thr Thr Leu Arg Thr Met Glu Asp Val Ile Ala Glu Gln Ser Val
                      295
                                           300
Ser Gly Tyr Phe Val Phe Cys Leu Gln Ile Ile Ile Ser Ile Gly Leu
                   310
                                       315
Met Phe Tyr Val Val His Arg Ala Gln Val Glu Leu Asn Ala Ala Ile
               325
                                   330
Val Ala Cys Glu Met Glu Leu Lys Ser Ser Leu Val Lys Gly Asn Gln
                               345
Pro Asn Thr Ser Gly Ser Ser Phe Tyr Asn Lys Arg Thr Leu Thr Phe
                           360
Ser Gly Gly Ile Asn Val Val
   370
```

<210> 2

```
<211> 1143
 <212> DNA
 <213> mouse
 <400> 3
 atgcggaacc ccggtgggag cctgcccac acgctgcccc gggccttgca gcacgccggt 60
 cggacgggag tcgtggagca gccgggccgc tgggcaccgg agcggacagc gggaggggac 120
 cgctcggagg accgccttcc ccgcgggggc ggggccagcg cggcggcggc tgctgctgcg 180
 gcggcggcct cgggcgccct gctcggcgcc tatctggagc gccacggtct gcccgcggcc 240
 teggaettge eggegeegge eggggegttg geaggegge eegggagegg eggeggegtg 300
 gtggtcgggg tggccgaggt gagaaactgg cgctgctgct gcctcggcag cacctgttgg 360
 tgccggagcc tcgtgctggt gtgcgtgctg gccgccctgt gcttcgcttc cctggccctg 420
 gtccgccgct acctgcagca cctcctgctc tgggtggaga gcctcgactc gctgctcggt 480
 gtcctgctct tcgtcgtggg cttcatcgtg gtctccttcc cctgcggttg gggctacatc 540
 gtgcttaatg tggcggccgg ctacctgtac ggcttcgtgc taggcatggg gctcatggtg 600
 gtgggcgtcc tcattggcac ctttatcgct catgtggtct gcaagcggct actcaccgcc 660
 tgggtggctg ccaggatcca gaacagcgac aagctgagcg ccgttatccg cgtcgtggag 720
 ggaggaagcg gcctgaaggt ggtggcgctg gcccggctga ctcccatacc ttttgggctt 780
 cagaatgcag tgttttcgat tactgacgtc cccttgccca gctacctgat ggcgtcttca 840
 gctgggctgc tcccgactca gcttctgaat tcttacttgg gaaccacact acggactatg 900
 gaagatgtca tcgcagaaca aagtcttagt ggctattttg tcttttgttt acagattgtt 960
ataagcattg gcctcatgtt ttatgtagtc catcgcgctc aagtggaatt gaatgcagct 1020
attgtagctt gtgagatgga actgaaaacc tctctggtta aaggcaatca atcggatccc 1080
agtggctctt ccttctacaa caagaggacc ctcacgtttt ctggaggtgg aatcaatatt 1140
gta
 <210> 4
<211> 381
<212> PRT
<213> mouse
<400> 4
Met Arg Asn Pro Gly Gly Ser Leu Pro His Thr Leu Pro Arg Ala Leu
                                     10
Gln His Ala Gly Arg Thr Gly Val Val Glu Gln Pro Gly Arg Trp Ala
                                 25
Pro Glu Arg Thr Ala Gly Gly Asp Arg Ser Glu Asp Arg Leu Pro Arg
                             40
Gly Gly Gly Ala Ser Ala Ala Ala Ala Ala Ala Ala Ala Ala Ser
                        55
Gly Ala Leu Leu Gly Ala Tyr Leu Glu Arg His Gly Leu Pro Ala Ala
Ser Asp Leu Pro Ala Pro Ala Gly Ala Leu Ala Gly Gly Pro Gly Ser
                85
Gly Gly Val Val Val Gly Val Ala Glu Val Arg Asn Trp Arg Cys
                                105
                                                    110
Cys Cys Leu Gly Ser Thr Cys Trp Cys Arg Ser Leu Val Leu Val Cys
                            120
Val Leu Ala Ala Leu Cys Phe Ala Ser Leu Ala Leu Val Arg Arg Tyr
                        135
Leu Gln His Leu Leu Leu Trp Val Glu Ser Leu Asp Ser Leu Leu Gly
                    150
                                        155
Val Leu Leu Phe Val Val Gly Phe Ile Val Val Ser Phe Pro Cys Gly
                                    170
                                                        175
Trp Gly Tyr Ile Val Leu Asn Val Ala Ala Gly Tyr Leu Tyr Gly Phe
                                185
Val Leu Gly Met Gly Leu Met Val Val Gly Val Leu Ile Gly Thr Phe
        195
                            200
Ile Ala His Val Val Cys Lys Arg Leu Leu Thr Ala Trp Val Ala Ala
                        215
                                            220
```

<210> 3

Arg Ile Gln Asn Ser Asp Lys Leu Ser Ala Val Ile Arg Val Val Glu Gly Gly Ser Gly Leu Lys Val Val Ala Leu Ala Arg Leu Thr Pro Ile Pro Phe Gly Leu Gln Asn Ala Val Phe Ser Ile Thr Asp Val Pro Leu Pro Ser Tyr Leu Met Ala Ser Ser Ala Gly Leu Leu Pro Thr Gln Leu Leu Asn Ser Tyr Leu Gly Thr Thr Leu Arg Thr Met Glu Asp Val Ile Ala Glu Gln Ser Leu Ser Gly Tyr Phe Val Phe Cys Leu Gln Ile Val Ile Ser Ile Gly Leu Met Phe Tyr Val Val His Arg Ala Gln Val Glu Leu Asn Ala Ala Ile Val Ala Cys Glu Met Glu Leu Lys Thr Ser Leu Val Lys Gly Asn Gln Ser Asp Pro Ser Gly Ser Ser Phe Tyr Asn Lys Arg Thr Leu Thr Phe Ser Gly Gly Gly Ile Asn Ile Val